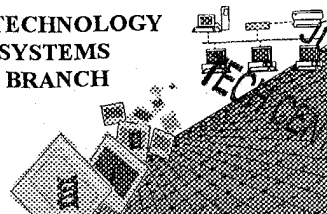


## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/724,678C  
Source: 1600  
Date Processed by STIC: 6/11/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

RECEIVED  
JUL 02 2002  
TECH CENTER 1600/2900

**ERROR DETECTED**

**SUGGESTED CORRECTION**

SERIAL NUMBER: 09/724,678c

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
    This sequence is intentionally skipped  
  
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
    <210> sequence id number  
    <400> sequence id number  
    000
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ✓ Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>      Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n      n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



1600

## RAW SEQUENCE LISTING

DATE: 06/27/2002

PATENT APPLICATION: US/09/724,678C

TIME: 19:09:33

Input Set : N:\AMC\Sequence Listing.txt

Output Set: N:\CRF3\06272002\I724678C.raw

pp1-3  
Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Lee, Kang-Hung  
4 Bair, Chi-Horng  
5 Tseng, Yang-Yuan  
6 Wang, Yih-Weng  
7 Wang, Shing-Hwan  
9 <120> TITLE OF INVENTION: Methods for Detecting and differentiating Enteroviruses and  
the Primers  
10 and Probes Therefor  
12 <130> FILE REFERENCE: TAI 3L6  
14 <140> CURRENT APPLICATION NUMBER: 09/724,678C  
15 <141> CURRENT FILING DATE: 2000-11-28  
17 <160> NUMBER OF SEQ ID NOS: 16  
19 <170> SOFTWARE: PatentIn version 3.1  
21 <210> SEQ ID NO: 1  
22 <211> LENGTH: 16  
23 <212> TYPE: DNA  
24 <213> ORGANISM: synthetic construct  
26 <400> SEQUENCE: 1  
27 ttgttcgcct gtttta  
30 <210> SEQ ID NO: 2  
31 <211> LENGTH: 21  
32 <212> TYPE: DNA  
33 <213> ORGANISM: synthetic construct  
35 <400> SEQUENCE: 2  
36 caagcacttc tgthccccg g  
39 <210> SEQ ID NO: 3  
40 <211> LENGTH: 19  
41 <212> TYPE: DNA  
42 <213> ORGANISM: synthetic construct  
44 <400> SEQUENCE: 3  
45 tacttcgaga arccyagta  
48 <210> SEQ ID NO: 4  
49 <211> LENGTH: 17  
50 <212> TYPE: DNA  
51 <213> ORGANISM: synthetic construct  
53 <400> SEQUENCE: 4  
54 aagagyctat tgagcta  
57 <210> SEQ ID NO: 5  
58 <211> LENGTH: 20  
59 <212> TYPE: DNA  
60 <213> ORGANISM: synthetic construct  
62 <220> FEATURE:  
63 <221> NAME/KEY: misc\_feature  
64 <222> LOCATION: (3)..(3)

(global)  
invalid response - see item 10 on Error  
Summary Sheet

16  
21  
19  
17

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/724,678C

DATE: 06/27/2002

TIME: 19:09:33

Input Set : N:\AMC\Sequence Listing.txt

Output Set: N:\CRF3\06272002\I724678C.raw

65 <223> OTHER INFORMATION: n = inosine  
68 <220> FEATURE:  
69 <221> NAME/KEY: misc\_feature  
70 <222> LOCATION: (18)..(18)  
71 <223> OTHER INFORMATION: n = inosine  
74 <400> SEQUENCE: 5  
W-5 75 ggntggtrst ggaarttnc 20  
78 <210> SEQ ID NO: 6  
79 <211> LENGTH: 19  
80 <212> TYPE: DNA  
81 <213> ORGANISM: synthetic construct  
83 <400> SEQUENCE: 6  
84 cacyggatgg ccaatccaa 19  
87 <210> SEQ ID NO: 7  
88 <211> LENGTH: 20  
89 <212> TYPE: DNA  
90 <213> ORGANISM: synthetic construct  
92 <400> SEQUENCE: 7  
93 attgtcacca taagcagcca 20  
96 <210> SEQ ID NO: 8  
97 <211> LENGTH: 20  
98 <212> TYPE: DNA  
99 <213> ORGANISM: synthetic construct  
101 <220> FEATURE:  
102 <221> NAME/KEY: misc\_feature  
103 <222> LOCATION: (6)..(6)  
104 <223> OTHER INFORMATION: n = inosine  
107 <220> FEATURE:  
108 <221> NAME/KEY: misc\_feature  
109 <222> LOCATION: (18)..(18)  
110 <223> OTHER INFORMATION: n = inosine  
113 <400> SEQUENCE: 8  
W-6 114 arrttnatcc aytgrtgngg 20  
117 <210> SEQ ID NO: 9  
118 <211> LENGTH: 27  
119 <212> TYPE: DNA  
120 <213> ORGANISM: synthetic construct  
122 <400> SEQUENCE: 9  
123 tcctccggcc cctgaatgcg gctaate 27  
126 <210> SEQ ID NO: 10  
127 <211> LENGTH: 33  
128 <212> TYPE: DNA  
129 <213> ORGANISM: synthetic construct  
131 <400> SEQUENCE: 10  
132 tgtcgtaacg sgcaastcyg yrgcgggaacc gac 33  
135 <210> SEQ ID NO: 11  
136 <211> LENGTH: 28  
137 <212> TYPE: DNA  
138 <213> ORGANISM: synthetic construct

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/724,678C

DATE: 06/27/2002

TIME: 19:09:33

Input Set : N:\AMC\Sequence Listing.txt

Output Set: N:\CRF3\06272002\I724678C.raw

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140 <400> SEQUENCE: 11
141 tactttgggt gtccgtgttt chttttat 28
144 <210> SEQ ID NO: 12
145 <211> LENGTH: 30
146 <212> TYPE: DNA
147 <213> ORGANISM: synthetic construct
149 <400> SEQUENCE: 12
150 cttataagca gactcaaccc ggtgctgatg 30
153 <210> SEQ ID NO: 13
154 <211> LENGTH: 28
155 <212> TYPE: DNA
156 <213> ORGANISM: synthetic construct
158 <400> SEQUENCE: 13
159 tggcattcca atatcacaat taacagtg 28
162 <210> SEQ ID NO: 14
163 <211> LENGTH: 30
164 <212> TYPE: DNA
165 <213> ORGANISM: synthetic construct
167 <400> SEQUENCE: 14
168 ctcggcacta tcgcaggagg gaccgggaat 30
171 <210> SEQ ID NO: 15
172 <211> LENGTH: 30
173 <212> TYPE: DNA
174 <213> ORGANISM: synthetic construct
176 <400> SEQUENCE: 15
177 cctacgccac tacacagcct ggtcaggttg 30
180 <210> SEQ ID NO: 16
181 <211> LENGTH: 1560
182 <212> TYPE: DNA
183 <213> ORGANISM: Enterovirus 71
185 <400> SEQUENCE: 16
186 ttaaaacagc tgtgggttgt caccaccca cagggtccac tgggcgctag tacactggta 60
188 tctcggtacc ttgtacgcc tgttttatac cccctccctg atttgcaact tagaagcaac 120
190 gcaaaccaga tcaatagtag gtgtgacata ccagtcgcat cttgatcaag cacttctgta 180
192 tccccggacc gagtatcaat agactgtgca cacggttgaa ggagaaaacg tccgttaccc 240
194 ggctaactac ttcgagaagc ctagtaacgc cattgaagtt gcagagtgtt tcgctcagca 300
196 ctccccccgt gtagatcagg tcgatgagtc accgcattcc ccacgggcca cgtggcggt 360
198 ggctgcgttg gcggcctgcc tatggggtaa cccataggac gctctaatac ggacatggcg 420
200 tgaagagtct attgagctag ttagtagtcc tccggccccct gaatgcggct aatcctaact 480
202 gcggagcaca tacccttaat ccaaagggca gtgtgtcgta acgggcaact ctgcagcga 540
204 accgactact ttgggtgtcc gtgtttcttt ttattcttgt attggctgct tatggtgaca 600
206 attaaagaat tgttaccata tagctattgg attggccatc cagtgtcaaa cagagctatt 660
208 gtatatctct ttgttgatt cacacctctc actcttgaaa cgttacacac cctcaattac 720
210 attatactgc tgaacacgaa gcgatgggct cccagggtctc cacacagcga tccggctcgc 780
212 atgagaattc caactcagcc acggaaggct ccactataaa ttacacaacc attaattact 840
214 acaaagactc gtatgctgcc actgctggaa agcaaagtct caaacaagat cctgacaagt 900
216 ttgcgaaccc tgtgaaggac atctttactg aaatggcagc gcccttaaag tctccctctg 960
218 ctgaagcatg tggctatagc gaccgagtgg cacagcttac cattggaaat tccaccatta 1020
220 ctacacaaga agcagcaaac ataatagttg ggtatggtga gtggccttca tactgctctg 1080

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## RAW SEQUENCE LISTING

DATE: 06/27/2002

PATENT APPLICATION: US/09/724,678C

TIME: 19:09:33

Input Set : N:\AMC\Sequence Listing.txt

Output Set: N:\CRF3\06272002\I724678C.raw

|     |            |             |            |            |            |            |      |
|-----|------------|-------------|------------|------------|------------|------------|------|
| 222 | ataatgatgc | aacagcggta  | gacaaaccta | cacggcctga | tgtctcagta | aatagatttt | 1140 |
| 224 | acacgctaga | cactaagcta  | tgggagaaat | catccaaggg | gtggtactgg | aagttcccag | 1200 |
| 226 | atgtactgac | tgaaaccgga  | gtttttggtc | caaatgcaca | atttcactac | ttataccggt | 1260 |
| 228 | cagggttctg | catccacggt  | caatgtaacg | ctagcaaatt | tcaccaaggg | gcgctactcg | 1320 |
| 230 | ttgcggtatt | gcccagagtat | gtcattggaa | cagtggcagg | cggcacaggc | acagagaaca | 1380 |
| 232 | gtcaccctcc | ttataaaca   | acccaacccg | gcgctgatgg | atttgaatta | caacatccat | 1440 |
| 234 | atgttcttga | tgctggaatt  | ccaatatctc | agttgacagt | gtgccctcac | cagtggatca | 1500 |
| 236 | atttacgaac | caacaattgt  | gccaccataa | tagtgccata | catgaacaca | ctaccttttg | 1560 |

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/09/724,678C

DATE: 06/27/2002  
TIME: 19:09:34

Input Set : N:\AMC\Sequence Listing.txt  
Output Set: N:\CRF3\06272002\I724678C.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 3,18

Seq#:8; N Pos. 6,18